

FIGURE 1A

Signal Peptide		Prodomain	
DKUZ	MSSKCAFNIVFVSIIIFIIVNGYAKDISGVKRGHERNEXISHYETIMVDHEHIRASNNRARRSVTK-DOYVHLK	74	
MKUZ	MLPTVLILLLSWAAGLGG--QYGNPKNKYIRHYEGLSYNVDLSLHQAQRAKRAVSHE	63	
DKUZ	FASHGRDFHLRLKRDINTSNKLDYDYSKGPIDVSDTHIYEVEGIVGDRNSYVFGSIHNGVFEFGKIITERDAYVVE	149	
MKUZ	FHAHGRQFNLRMKRDITSLFSEDFKVTENKVLQYDITSHIYTGHIYGEEGSFHSGSVIDGRFEGFKIRGGTFYIE	138	
DKUZ	HAKHYFPTNRTATITPPSTITSSATVTKSTQPTRPLAKSNTSTTAVNSKTENFIKIAESTTTSQALPEYTES	224	
MKUZ	PAERYIK-----	145	
DKUZ	SSSSSTTFPPTTEYFEDEKERNAEDELDFHSILYKESHVEDAYENVREGHVAGCGITDEVSQWMENIQNSAVEE	299	
MKUZ	-----DRIIPFHSVLYHEDDINYPHKYGPQGGCAD-----HSVFERMRKYQMTGVEE	192	
Metalloprotease Domain			
DKUZ	LPEPMSKDYQKLHRKQTHKKSAPQAAQPPPKKYSIGDEDFKYPHQKYTKEANFAEGAFYDPSTGRRRLGSSANV	374	
MKUZ	GARAHPKHAASSGPELRK-----	213	
DKUZ	ADWHLVHERVRRATDNGAGDRGSSGGSGRGREDNKNTCSLYIQIDPLIWRHIREGIAHDRGRKYEVDEKTREE	449	
MKUZ	-----RTTLAERNITGLYIQTDLHFFKY-----GTREA	242	
DKUZ	ITSLIAHVIYAVNYIYRNITKFDGRTEHRNIRFEVQRIKIDDSACRNSYNGPHNAFCNEHMDVSNFLNHSLEDH	524	
MKUZ	VIAQISSHVKAIDTLYQTIDESGI---RNISFMVKRIINTTIDEKD---PTNPFPPNIGVEKFLNLSLEGNH	310	
DKUZ	SDFCLAYVFTYRDFTGGLGLAWVASASGASGGICEKYKITYTETVGGYASTKRSNTGITITFVNYNSRVPPPKVS	599	
MKUZ	DDYCLAYVFTDRDFDDGLGLAWVGAPSGSSGGICEKSKLYSD-----GKKSLNTGITITVQNYGSHVPPPKVS	378	
Zn++			
DKUZ	QLTLAHEIGHNFGSPHDYPQEGRPGGGL-----NGNYIMFASATSGDRPNNSKFSPCSIERNISNVL DVLVGNTK	667	
MKUZ	HITFAHEVGHNFGSPHDSGTETPGESKNLGQKENNGNYIMYARATSGDKLNNKFSLSIERNISQVLE---KKR	449	
Disintegrin Domain			
DKUZ	RDGFKASEGAFCGNKIVESGEECDGCFNEEECKDKCCYPRLISEYDQSLNSSAKGCTRRAKIQCSPSQSGPCCLSN	742	
MKUZ	NNCFVESGQPICGNGMVEGEECDGCGYSDQ-CKDDCCF-----DANQPEGKKCKLKPQKQCSQSGPCC-IA	514	
XKUZ	-----YSDQ-CKDECCY-----DANQPENLKCTLKPGKQCSQSGPCC-IT	39	
Cysteine-rich Domain			
DKUZ	SCTFVPTSYHQKCKEETECSSHSSTCNGTITACEPEPRHRDDKIMCNGTALCIRGECGSGSPCLLNNMIKCFLTSTT	817	
MKUZ	QCAFKSKS--EKCRDSDCAKMGTCNGNSAQCPPSEPRENLIE-NRAIQVCIKGQCSGSICERYDLEEC--TCAS	585	
XKUZ	GCTFKRAG--ENCREESDCAKMGTCNGNSAQCPPSEPRENLIE-NRAIQVCIKGQCSGSICERYDLEEC--TCGS	109	
DKUZ	LPHVSKRKICDLACQDNDITCRSTSEFADKYNIAQKGGTISLQPGSPCDNFQGYCDVFLKCRAVDADGGLRLKN	892	
MKUZ	SDGKDNKELCHVCCMKMASTICASTGSLQMSKQFSGRITTLQPGSPCDNFRGYCDVFMRCRLVDADGGLRLKK	660	
XKUZ	TDEKDKELCHVCCMEKMIPIHTCASTGSEVWKAAYFKGKTIILQPGSPCNEFK	161	
Transmembrane domain			
DKUZ	LLLNRKTLQTVAEWIVDNWYLVVWGVAFIVVWGSFIKCCAVHIPSSNPKKRRARRISEILLRAPMNTLRRMQRHP	967	
MKUZ	AIFSPQLYENIAEWIVAHMVAVLIMGIALIMLMAGFIKICSVHTPSSNPKLPPPKPLPGLK-----RRRPP	727	
DKUZ	NQRGAGPRSIPPPAHEAQHYSRGGDGRGGGGGGGGRRHGGSRSHQAHPHDWRHQGGHSIVPLPTGGSHSRNSA	1042	
MKUZ	QPIQQPPRQRPRESYQMGHMR	749	
DKUZ	ANQARRSDGRPRSTSSGRPQAIASGSGAASGAARSHGGYGAEQAI PGSIGGGVQAAISSGGVVARAQLPLPLPP	1117	
DKUZ	PNGQQQMQQQQQLLQAPPAISPPQQPQAQFYTPKELPPRNKSRSSRTNNTSTTTTNSSTAAGSGSVSGPGSG	1192	
DKUZ	AGSSSKSKSGKSAKAKDSKQSQQAANNSRSSSKKEKGKVPVRNIV	1239	

FIGURE 1A

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

FOFES0" 88EF4860

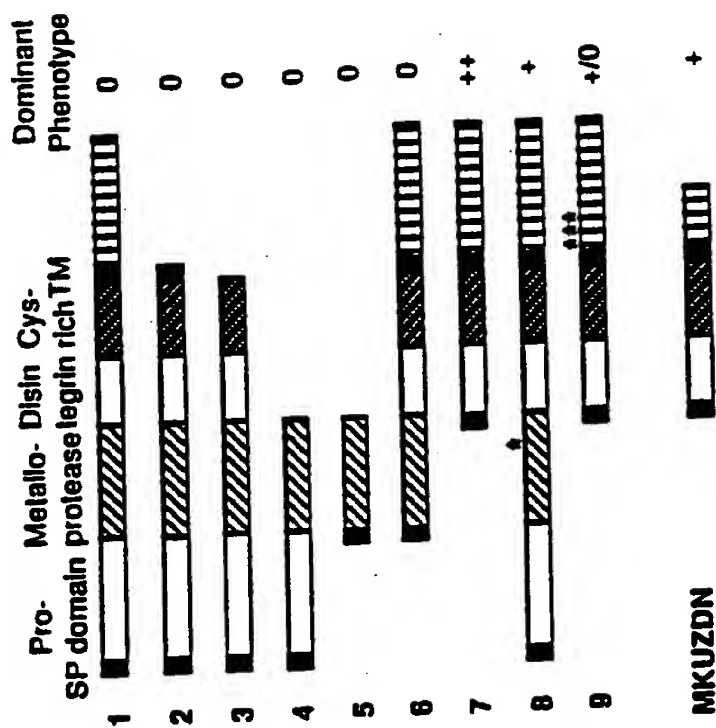


FIGURE 1 B

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

TTESD" BBEF2860

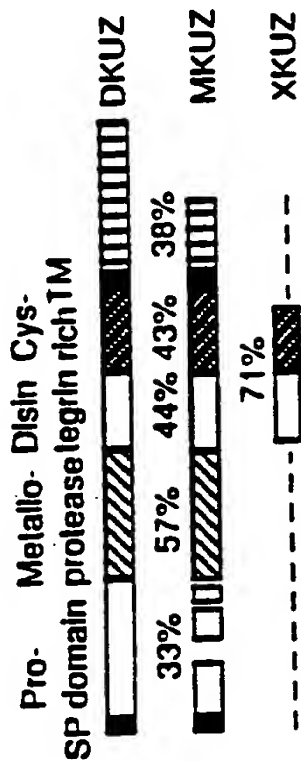


FIGURE 1 C

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

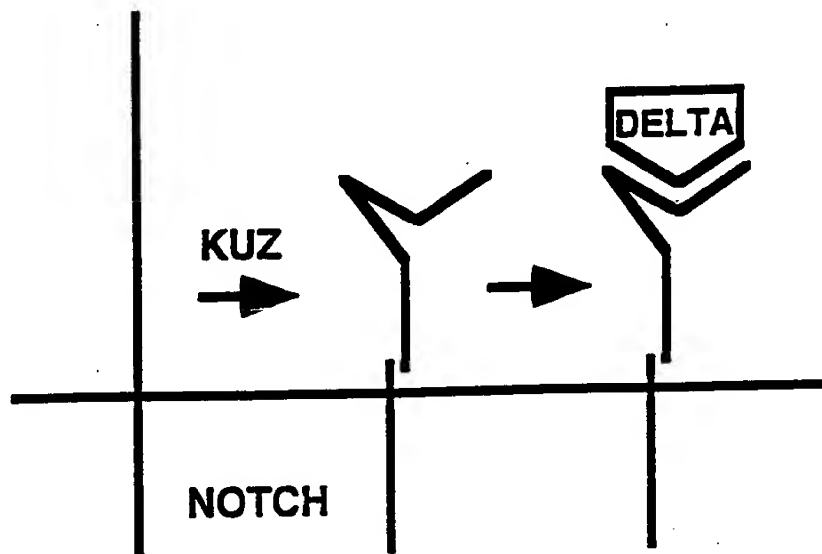


FIGURE 2

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